

Structural and Functional Diversity of β -Adrenergic Receptors^a

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Recent progress in molecular cloning techniques has allowed the identification of the genes or cDNAs corresponding to proteins homologous to but different from previously known receptors. These "new" sequences have since been shown to encode subtypes whose existence had been suspected on the basis of pharmacologic data. A good example of such a new subtype is the β_3 -adrenergic receptor (β_3 AR). Its gene was first cloned by homology using β_2 - and β_1 -specific DNA oligonucleotide probes.¹ Corresponding β_3 species homologues were later cloned from mouse² and rat.^{3,4} After transfection of the β_3 AR gene in Chinese hamster ovary (CHO) cells, which are devoid of such receptors, it was shown that the β AR subtype displays most of the ligand-binding and adenylyl cyclase-stimulating properties of previously described "atypical" receptors in various rodent species (reviewed in refs. 5 and 6).

The β_3 AR is quite distinct from the β_1 - and β_2 AR and thus presents an interesting case of diversity in the small family of β ARs.⁷ In this paper we discuss the various features that distinguish the three β AR subtypes.

MOLECULAR DIFFERENCES

All three β ARs belong to the R₇G superfamily of receptors coupled to GTP binding proteins.⁸ They are thus composed of a single polypeptide chain with seven putative transmembrane domains, an extracellular glycosylated N-terminal and an intracellular C-terminal region (FIG. 1). As in all other R₇G proteins, the β AR subtypes vary extensively both in terms of length and sequences in the N- and C-terminal as well as in the third intracellular (i3) regions (FIG. 2). Although the seven hydrophobic regions are quite conserved, a number of differences may explain the striking pharmacologic and regulatory variations.

The degree of amino acid sequence identity between man, mouse, and rat β_3 AR (FIG. 2) is much higher (80–90%) than that existing between different β AR subtypes

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(40–50%) and is of the same order as that observed across species for a given receptor subtype. Several residues located in the functional domains of the receptor are specifically shared by the human, murine, and rat β_3 AR, but are not found in the β_1 - and β_2 AR sequences. From a genetic point of view, the human, mouse, and rat β_3 AR genes all display a similar genomic organization with an intron interrupting the 3' end of the coding block,^{9–12} whereas the other β AR subtypes are intronless. Moreover, the human and mouse genes have been assigned to a chromosomal linkage group which is conserved between the two species.² Together, these structural data strongly suggest that the human, mouse, and rat genes do not encode distinct β AR subtypes,⁴ but are species homologues of the β_3 AR gene.

A number of residues found in human β_1 - and β_2 AR sequences are substituted by residues that appear to be specific for β_3 . Most of these residues are found in all β_3 -receptors sequenced so far. Some of the changes appear to be selective for the human β_3 . Last, but not least, the Ser/Thr phosphorylation target sites documented for β_1 - and β_2 ARs are absent from all β_3 . The rodent β_3 ARs appear to share with the human β_3 quite a number of structural features that distinguish this subtype from β_1 and β_2 . There are, in addition to these β_3 -specific substitutions, a number of rodent specific changes, as is the case, for example, for the Val Ala Leu deletion in the tm1 domain.

PHARMACOLOGIC DIFFERENCES

Five major features distinguish the human β_3 AR from those of β_1 and β_2 : (1) atypically low affinity for conventional β -antagonists including reference radioligands; (2) atypically low stereoselectivity index for agonist and antagonist enantiomers; (3) atypically low potencies of reference agonists; (4) high potency of a novel class of compounds initially described as potent activators of lipolysis and thermogenesis in white and brown adipose tissues of rodents; and (5) partial agonistic activities of several β_1/β_2 -antagonists, reflecting intrinsic sympathomimetic activities in tissues. Such general properties are reminiscent of those ascribed to the atypical β AR initially proposed to exist in adipose tissues and later in the digestive tract of rodents. These tissues are also the only ones where β_3 mRNA expression was unambiguously demonstrated both in human¹³ and rodents.^{2,3,12}

The rodent β_3 again appears to be somewhat different from the human subtype: in CMO β_3 cells, propranolol is an antagonist for mouse β_3 , as it is for β_1 and β_2 , in contrast to what is seen in the human β_3 where it behaves as a weak agonist. A number of other compounds display either stronger or weaker effects in the β_3 human or rodent without any obvious trend: BRL 37344, for example, approximately 30 times more potent in the rodent, whereas carazolol is about 8 times more potent in the human β_3 .

FIGURE 1. Primary structure of the human β_3 AR. The sequences are represented in the one-letter code for amino acids. The single polypeptide chain is arranged according to the model for rhodopsin. The disulfide bond essential for activity Cys¹¹¹ and Cys¹⁰⁹ is represented by -S-S-. The two N-glycosylation sites in the amino-terminal portion of the protein are indicated by ∇ . The palmitoylated Cys³⁶⁰ residue in the N-terminus of the i4 loop is indicated by the symbol ξ .

	e1	tm1	i1	
Mo83	MAPWPHRNGSLALWSDAPTLDP	SAANTSGLP	GVFWAAALAGALLALA	TVGGNLLVIIAIARTPRLQITINVFVTSL
Ra83	M-----K-----F-----	-----T-----		
Hu83	M-----E-S-----P-P-L-----A-NT-----E-----	VLA-----V-----W-----M-----		
Hu81	MGAGVLVLGASEP	GNLSSAAPLPDGAATAAR-LVPASP-ASLLPP-SESPE-LSQQWT-GM-L-M--IVLLI-A--V--V--K-----L--L-IM--		
Hu82		MGQPGNGSAFL--NGSHAPDHVDTQQRDEVVWV-M-IVMS-IVLAI-F--V--T--KFE--V--Y-I--		
	tm2	e2	tm3	i2
Mo83	AAADLVVGLLVMPGATLALTGHWPLGETGCELWTSVDVLCVTASITETLCALAVD		DAVTNELRYGTLVTKRRARA	AVLVWIVSAAVSFAPIMSQWR
Ra83	-T-----A-----			
Hu83	-M-----V--A-----A-----		A-----C--T-----V-----	
Hu81	-S--M--V-F--IVVW-R-EY-SFF-----VI-I-----I-S--QS-L-RA--GL-CT--AI--L--L--LMH--			
Hu82	-C--M--A-V-F--AHI-MKM-TF-NFW-F--I-----VI--F-I-S-EK-QS-L-NK--VIIILM--GLT--L--QMH-Y-			
	e3	tm5	i3	
Mo83	VGADAEAECHSNPRCCSFASNMPYALLSSVSFYLPLLVMLFVYARVFAKRRHLLRRELGRF		SPEESPSPSRSPSPATGGTPAAPD	
Ra83	-----R-----A-----V-----		P-----R-----V--T-S-	
Hu83	-----R-----A-----V-----		T-LR--G--P-----LA--PV--C-P-E	
Hu81	AES--RR-YND-K--D-VT-RA--IA--V--V--CI-A--L--RE-QK-VKKIDSCER--LGGPAR--S--P--V--PAPP-G--RPAAAAATA			
Hu82	ATHQ--IN-YA-ET--DFFT-QA--IA--I--V--VI-V--S--QE--LQKIDKSE--HVQNL-QVEQ			
	tm6	e4	tm7	
Mo83	GVPPCGRRPARLLPLREHRLRTLGLIMGIFSLCWLPPFLANVLRALAGPSLVPSGVFIALNWLGYANSFNPVIYCHPTVADNTPFANFYGGRG			
Ra83	--S-----G-----V-----L-----			
Hu83	--A-----C-----T-T-----G-----GPA-L-----L-----S-----TG-R-L			
Hu81	PLANGRAGK--S--VA--QK--K--I--V-T-----VK-FHRE--DRL-VFF-----I-----CARRAA			
Hu82	DGRTGHGL--SSKP C-K--K--K--I--T-----IV-IVHVIQDN--IRKE-Y-L--I--V--G--L-----RRSSL			
	i4			
Mo83	PEEPRAVTFPASPVEARQSPPLNRFDCYEGARPFPT			
Ra83	-----V-----AS--NS-----E-----			
Hu83	-P--C--AAR--LFPSGVPAARSSPAQPRLCQRLDGASWGS			
Hu81	RRRHATHGDRPRASGCLARPGPP-SPGAASDDD-DDVVGATPPARLLEPWAGCNGGAADSSSLDEPCRPGFASESQV			
Hu82	KAYNGYSSNGNTGEQSGYHVEQEKENK-LCEDLPGTEDFVGHQGTVPDNDISQGRNCSTNDSLL			

DIFFERENT CONTROL MECHANISMS REGULATE β_1 -, β_2 - AND β_3 AR EXPRESSION

A variety of control mechanisms regulate the function and expression of the β AR subtypes. We summarize in TABLE 1 a few of the factors involved in β AR regulation, and show the differences between β_1 , β_2 , and β_3 .

Agonist-induced Desensitization

One of the most specific mechanisms is desensitization, a complex physiologic process, which prevents the hormonal overload of most G-protein-coupled receptors by impairing the signal-transmission pathway at receptor and/or postreceptor levels. An important clinical consequence of desensitization is the relative or complete resistance to pharmacologic agonists given for an extended period of time.

Several molecular mechanisms involved in receptor desensitization have been characterized for the β_2 AR.¹⁴ After a few minutes of receptor activation by an agonist, phosphorylation of β_2 AR by protein kinase A (PKA) and β AR kinase (β ARK) results in the rapid uncoupling of the receptor from the transducing pathway.^{15,16} Phosphorylation by PKA is a negative-feedback of receptor activation, mediated by the raise of intracellular cAMP, which affects all β_2 AR, whereas β ARK phosphorylates only those receptors that are occupied by the agonist.¹⁷ When receptor activation is sustained for longer periods of time (hours), protein degradation of preexisting receptors and destabilization of the receptor mRNA contribute to the reduction of the total number of β_2 AR (i.e., receptor down-regulation).¹⁸

The three β AR subtypes are not equally sensitive to desensitization. The β_1 AR, which has fewer potential phosphorylation sites and lacks the two tyrosine residues implicated in the down-regulation of the β_2 AR,¹⁹ is less prone than the β_2 AR to both short-term²⁰ and long-term²¹ desensitization. The third β AR subtype is almost completely resistant to short-term desensitization,^{12,22} primarily because this receptor does not undergo PKA- or β ARK-induced phosphorylation—most likely because of the absence of the target sequences identified on the β_2 AR.⁸

Other Mechanisms for β AR Modulation

A number of other compounds and factors have been shown to affect β AR expression and function (TABLE 1). These include glucocorticoids, butyrate, insulin adipocyte differentiation, and cold. The three β ARs are diversely affected by these different conditions, again demonstrating that each subtype is regulated independently and may thus play a distinct physiologic role.

FIGURE 2. Amino acid sequence comparison of the mouse (Mo), rat (Ra), and human (Hu) β_1 -, β_2 -, and β_3 ARs. The seven transmembrane segments (tm1–tm7) are boxed and alternate with extracellular (e1–e4) and intracellular (i1–i4) domains. Gaps (horizontal dashes) have been introduced to maximize sequence alignment. Black triangles indicate residues conserved in all nine proteins, and dots represent classical substitution according to Daihoff PAM 250 matrix.

CONCLUSION

The comparison of the three β AR subtypes reveals both striking structural similarities, especially in the ligand binding and G-protein interacting sites, and important differences. These concern mainly regulatory control of receptor expression and function. It is likely that other families of receptor subtypes will display similar features by which binding of the same natural ligands may result in widely different functional effects, well controlled by developmentally or hormonally regulated mechanisms.

SUMMARY

The molecular and functional properties of the three β AR subtypes appear to be quite diversified even though all three bind the same natural catecholamines, adrenaline and noradrenaline, couple apparently to the same G_s transducer protein, and stimulate the same adenylyl cyclase effector. Binding characteristics for a variety of synthetic ligands thus encompass a wide range of K_d values, and a number of β_1/β_2 antagonists turn out to be potent agonists towards the β_3 subtype.

TABLE 1. Differential Up- and Down-Regulation of the Three β -Subtypes

Factors	β_1	β_2	β_3	References
Adipose differentiation	↓	↓	↑	Fève <i>et al.</i> ^{23,24}
cAMP	↓	↓	↑	Thomas <i>et al.</i> ²⁵
Dexamethasone	↓	↑	↓	Fève <i>et al.</i> ^{23,26}
Butyrate	↑	↑	↓	Krief <i>et al.</i> ²⁷
Insulin	→	→	↓	Fève <i>et al.</i> ²⁸

Regulatory mechanisms also appear to vary considerably from one β -receptor to another, with dexamethasone, for example, up-regulating the β_2 and down-regulating the β_1 and β_3 subtypes. Most striking is the fact that the β_3 subtype is resistant to the agonist-induced short-term desensitization initiated for the β_2 receptor by phosphorylation target sequences absent in β_3 .

Diversity in the three β AR subtypes clearly suggests different functional roles in the various tissues in which these receptors are expressed together or alone.

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